

Development and Genetic Analysis of Common Wheat Introgressive Lines Resistant to Leaf Rust

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Transfer of genetic material from tetraploid species, *Triticum timopheevii* Zhuk, resistant to diseases into common wheat *Triticum aestivum* L. has been carried out. Six common wheat cultivars were used. The process of hybrid forms stabilization have been studied in details; identification of *Triticum timopheevii* genetic material in genome of introgressive lines ($2n = 42$) resistant to leaf rust (*Puccinia triticina* Erikss.) has been carried out. Donors of rust resistance have been developed and the genetic control of the character has been studied. The resistance of obtained lines has been shown to be due to *Lr* genes, non-allelic to effective *Lr* genes from world collection.

Keywords: *Triticum timopheevii* Zhuk, introgressive lines, common wheat, resistance to leaf rust.

Development of cultivars resistant to diseases – one of the principal directions in up-to-date breeding. Wheat, being one of the main agricultural crops, is subjected to a considerable yield lost (30–50%) after diseases attack in epiphytotic years. Every year lost only from rust consists 5–10% (Mikhailova and Gultjaeva, 1998).

The most reliable and ecologically safe method of disease control is breeding and growing of resistant cultivars. Among common wheat relatives, in the world centers of its origin, several species are available, carrying the genes of resistance to diseases. Literature data indicate of many attempts to transfer such genes into commercial cultivars (Dvorak, 1977; Knott and Dvorak, 1981; Sears, 1981; Gill and Raupp, 1987, etc.). Use of chromosome manipulation allowed to enrich essentially the wheat germplasm with resistant genes. But the resistant forms on the genetic base of different cultivars have been derived sufficiently accident.

The main aim of our investigation was to use the unique pool of resistant genes in tetraploid endemic species, *Triticum timopheevii* Zhuk and making it available for resistance breeding. For this purpose, it was necessary to develop the collection of stable introgressive lines of common wheat with chromosome number $2n = 42$, with expression of *Triticum timopheevii* Zhuk resistance genes and with considerable number of characters similar to common wheat. These donor lines may serve as a constant source of “needed” genes in breeding process.

Materials and Methods

The direct transfer of *Triticum timopheevii* Zhuk (genome formula AAGG, $2n = 28$) genes through hybridization is hampered because of poor crossability with common

wheat *Triticum aestivum* L. (genome formula AABBDD, $2n = 42$), sterility of F_1 hybrids and instability of hybrids in early generations.. Only single backcrossing of F_1 hybrids with initial cultivar was used followed by self-pollinating. As recipients of *Triticum timopheevii* Zhuk (*T.t*) genetic material, six commercial common wheat cultivars were used: Saratovskaya 29 (S29), Novosibirskaya 67 (N67), Pyrotrix 28 (P28), Skala (Sk), Irtyshanka (Irt) and Tselinnaya 20 (Ts20). Hybrid plants in population derived from crossing of these cultivars as a female parent with *Triticum timopheevii* Zhuk were studied cytogenetically in F_1B_1 – F_7B_1 generations. Cytologically stable plants were picked out, resistant to a field population of leaf rust which is rather constant in Siberian conditions (Mikhailova and Tyryshkin, 1994). Mains-Jackson scale of immunity was used for evaluation of resistance.

For identification of *Triticum timopheevii* Zhuk genetic material transferred into common wheat the following methods have been used: C-banding technique, method of biochemical markers (Kalinina et al., 1987) and molecular markers (Leonova et al., 1999). The every year strict evaluation of resistance to rust was carried out for introgressive lines and their hybrids with initial and tester lines.

Results and Discussion

Earlier we discussed the possibility to obtain wheat lines resistant to diseases after crossing of three cultivars with *Triticum timopheevii* Zhuk (Budashkina, 1988). Further comparative investigations of hybrid populations (F_1B_1 – F_7B_1) derived from crossing of six cultivars with this species, have shown the considerable influence of recipient genotype on intensity of genetic material transfer (Shkutina et al., 1998).

Using of biochemical markers have allowed to identify 9 from 14 chromosomes of *Triticum timopheevii* Zhuk haploid set (Kalinina et al., 1990). The following tendency have been established: the more chromosomes from two crossing species are engaged in bivalent pairing in F_1 hybrids, the more diversity of marked chromosome arms of donor species is presented in F_4B_1 offspring. Based on the data obtained the conclusion have been done that in the whole, the introgression of genetic material of *Triticum timopheevii* Zhuk goes effectively enough into this crossing combination. By C-banding of chromosomes in cytologically stable introgressive lines the transfer of alien genetic material has been shown to take place presumably according to the homology of entire chromosomes or their arms; translocations have been registered much more rarely (Badaeva et al., 1991). Chromosomes of the 7th homological group mostly were involved into rearrangements, of the 3rd – rather rarely.

Selection for resistance to rust have been made among the cytologically stable ($2n = 42$) lines picked out hybrid populations descended from different cross combinations. Data from *Table 1* demonstrated resistance to several races of both leaf and stem rust (Mikhailova, 1992, personal communication).

C-banding of resistance to leaf rust forms has shown that the greatest transfer was registered in 2nd and 6th homological group.

Table 1

Rust resistance in introgressive wheat lines

Variety, Line	Leaf rust							Stem rust							
	Populations			Races				Races					Populations		
	1*	2*	3*	15	25	77	192	11	17	21	34	40	117	2*	3*
S 29	4	3	3	–	4	4	4	4	4	4	4	4	3	4	4
753–1	0	0	0	0	0	0	0	0–2	0	0	4	x	0	3	3
778–3	0	0	0	0,1	0	0,1	0	–	4	0,2	0	4	3,4	0	3
797–1	0,1	0	0	0,1	0	0	0	4	0	0	4	3,4	4	3	3
829–1	0	1–2	1–2	0	0	0	0	x	0,1	0	0	–	–	0	3
842–2	0,1	0	0	0,1	0	0	0	x	3,4	0	0	4	0,2	1	2
<i>T. tim</i>	0	0	0	0	0,1	0	0	0,2	0–2	0	0,1	0	0,1	0,1	1

Notes: 1* – Novosibirsk; 2* – Derbent; 3* – Rostov
0, 1, 2 – resistance; 3, 4 – susceptibility

At present, there are about 80 introgressive lines in our collection, resistant to field population of leaf rust. Genetic analysis of their resistance is under study now (*Table 2*). This character has been shown to be under control of 1–2 genes with different

Table 2

Genetical analysis of leaf rust resistance in introgressive wheat lines

Line derivation	Number of line studied	Segregation pattern (res : susc) in the F ₂ hybrid populations (line X initial variety)							
		3 : 1	9 : 7	13 : 3	15 : 1	1 : 3	7 : 9	3 : 13	1 : 15
S 29 x T.t	28	–	8	–	–	10	10	2	1
N 67 x T.t	12	1	2	–	–	8	3	2	2
P 28 x T.t	15	–	–	–	–	4	–	5	6
Irt x T.t	14	9	3	–	3	–	1	–	–
Skala x T.t	5	2	1	2	1	1	1	–	–
Ts 20 x T.t	7	2	1	3	–	–	1	–	–
Σ	81	14	15	5	4	23	16	9	9

interactions between them. In some lines, the character of genetic control changes in dependence of season. Most of lines show the stability of resistance. Genetic analysis of sublines derived from some lines confirms this statement (*Table 3*).

Tests on allelism have shown that *Triticum timopheevii* Zhuk genes introgressed into common wheat providing it with resistance to the leaf rust are not allelic to known effective genes of world collection, such as *Lr9*, *Lr19*, *Lr23*, *Lr24* (*Table 4*).

Thus, the developed collection of introgressive lines may serve as a source of new genes for resistance to rust in common wheat breeding. Nowadays, the approaches are elaborating to map these genes on definite chromosomes.

Table 3Segregation in hybrid populations F₂ (subline x initial cultivar)

Cross combination	Phenotypes ratio (res :susc)		Segregation type	χ^2	P
	actual	theoretical			
157-2 x Sk	36 : 13	37 : 12	3 : 1	0.11	0.75–0.5
157-3 x Sk	27 : 7	21 : 7	3 : 1	0	
157-4 x Sk	34 : 8	32 : 10	3 : 1	0.53	0.5–0.25
157-5 x Sk	49 : 13	47 : 15	3 : 1	0.36	0.75–0.5
140-1 x Irt	19 : 48	17 : 50	1 : 3	0.32	0.75–0.5
140-2 x Irt	16 : 64	20 : 60	1 : 3	1.07	0.5–0.25
140-3 x Irt	26 : 39	28 : 37	1 : 3	0.25	0.75–0.5

Table 4Segregation in the F₂ hybrid populations (line x tester) for resistance (resistant : susceptible)

Line	Testers			
	Lr 9	Lr 19	Lr 23	Lr 24
811	82 : 7	36 : 15	19 : 45	87 : 3
78	59 : 13	42 : 33	52 : 36	62 : 25
747	69 : 6	67 : 11	62 : 11	67 : 10
673	24 : 10	61 : 12	25 : 24	63 : 13
692	66 : 9; 77 : 8	80 : 4	21 : 5	77 : 9
699	86 : 11	74 : 12	61 : 29	70 : 8; 77 : 8
640	78 : 3	61 : 7; 47 : 10; 66 : 11	39 : 26	67 : 4; 60 : 15
64	61 : 7	44 : 7	49 : 10	52 : 30
82	56 : 11	52 : 7	50 : 7	53 : 0
191	50 : 9	51 : 3	49 : 4	65 : 3
141	67 : 2	63 : 3	35 : 20	19 : 21

The size and position of introgressed *Triticum timopheevii* Zhuk fragments have been evaluated using microsatellite markers (SRR) (Leonova et al., 1999) in three resistant lines derived on the bases of S29 cultivar. SRR markers with known chromosome localization in common wheat were used (Röder et al., 1998). It was shown that in all three lines the large parts of 2A and 2B chromosomes are involved in substitution.

The resistance in these lines may be due to *Triticum timopheevii* Zhuk genes introgressed in 2A and 2B chromosomes. This is in agreement with literature data in the localization of considerable number of genes in chromosomes of 2nd homological group (McIntosh et al., 1995).

Further analysis of developed introgressive lines will allow to enlarge our knowledge about genetics of resistance and to enrich the genetic map of common wheat.

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